

REMARKS

Applicant maintains that the amendments introduce no new matter to the instant application. The amendments are requested to provide correct reference to Figures 3A-3C and 4A-4C.

Entry of the remarks made herein is respectfully requested.

Respectfully submitted,

MILLENNIUM PHARMACEUTICALS, INC.

By


JEAN M. SILVERI
Registration No. 39,030
75 Sidney Street
Cambridge, MA 02139
Telephone - (617) 679-7336
Facsimile - (617) 551-8820

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APPENDIX A CLEAN VERSION OF REPLACEMENT PARAGRAPHS

On page 6, please replace paragraphs [0026] and [0027] with the following:

A
[0026] *Figures 3A, 3B and 3C* depict alignments of regions of the 68730 protein to the top-scoring domains identified by searching for complete domains in PFAM (version 5.5) and SMART (version 3.1) against the HMM database (HMMER 2.1.1). Fig. 3A depicts an alignment of amino acid residues 23 to 279 of SEQ ID NO:2 with a protein kinase domain (PFAM Accession No. PF00069). A single domain was found, with a bit score of 346.3 and an E-value of 3.4e-100. Fig. 3B depicts an alignment of amino acid residues 23 to 279 of SEQ ID NO:2 with a serine/threonine kinase domain (SMART Accession No. S_TKc). The bit score is 386.6 and the E-value is 2.5e-112. Fig. 3C depicts an alignment of amino acid residues 23 to 279 of SEQ ID NO:2 with a tyrosine kinase domain (SMART Accession No. TyrKc). The bit score is 35.7 and the E-value is 4e-14. All three alignments show four underlined sequences. The first underlined sequence (at amino acid residues 29 to 57) is a pattern match to a protein kinase ATP binding region signature sequence (Prosite Accession No. PS00107). The second and third underlined sequences (at amino acid residues 109 to 116 and at amino acids 126 to 134) are pattern matches to Prosite Accession No. PS00007, a tyrosine kinase phosphorylation site. The fourth underlined sequence (at amino acid residues 140 to 152) is a pattern match to a serine/threonine protein kinase active site signature sequence (Prosite Accession No. PS00108).

[0027] *Figures 4A, 4B and 4C* depict alignments of the 69112 protein to the top-scoring domains identified by searching for complete domains in PFAM (version 5.5) and SMART (version 3.1) against the HMM database (HMMER 2.1.1). Fig. 4A depicts an alignment of amino acid residues 356 to 613 of SEQ ID NO:5 with a protein kinase domain (PFAM Accession No. PF00069). A single domain was found, with a bit score of 350.2 and an E-value of 2.3e-101. Fig. 4B depicts an alignment of amino acid residues 356 to 613 of SEQ ID NO:5 with a serine/threonine kinase domain (SMART Accession No. S_TKc). The bit score is 372.7 and the E-value is 3.8e-108. Fig. 4C depicts an alignment of amino acid residues 356 to 613 of SEQ ID NO:5 with a tyrosine kinase domain (SMART Accession No. TyrKc). The bit score is 50.0 and the E-value is 5.3e-15. All three alignments show an underlined sequence at 473 to 485, which is a pattern match to a serine/threonine protein kinase active site signature sequence (Prosite Accession No. PS00108).

APPENDIX B MARKED-UP VERSION OF REPLACEMENT PARAGRAPHS

On page 6, paragraphs [0026] and [0027] have been amended as follows:

[0026] *Figures 3A, 3B and 3C* depict alignments of regions of the 68730 protein to the top-scoring domains identified by searching for complete domains in PFAM (version 5.5) and SMART (version 3.1) against the HMM database (HMMER 2.1.1) Fig. [5A] 3A depicts an alignment of amino acid residues 23 to 279 of SEQ ID NO:2 with a protein kinase domain (PFAM Accession No. PF00069). A single domain was found, with a bit score of 346.3 and an E-value of 3.4e-100. Fig. [5B] 3B depicts an alignment of amino acid residues 23 to 279 of SEQ ID NO:2 with a serine/threonine kinase domain (SMART Accession No. S_TKc). The bit score is 386.6 and the E-value is 2.5e-112. Fig. [5C] 3C depicts an alignment of amino acid residues 23 to 279 of SEQ ID NO:2 with a tyrosine kinase domain (SMART Accession No. TyrKc). The bit score is 35.7 and the E-value is 4e-14. All three alignments show four underlined sequences. The first underlined sequence (at amino acid residues 29 to 57) is a pattern match to a protein kinase ATP binding region signature sequence (Prosite Accession No. PS00107). The second and third underlined sequences (at amino acid residues 109 to 116 and at amino acids 126 to 134) are pattern matches to Prosite Accession No. PS00007, a tyrosine kinase phosphorylation site. The fourth underlined sequence (at amino acid residues 140 to 152) is a pattern match to a serine/threonine protein kinase active site signature sequence (Prosite Accession No. PS00108).

[0027] *Figures 4A, 4B and 4C* depict alignments of the 69112 protein to the top-scoring domains identified by searching for complete domains in PFAM (version 5.5) and SMART (version 3.1) against the HMM database (HMMER 2.1.1) Fig. [6A] 4A depicts an alignment of amino acid residues 356 to 613 of SEQ ID NO:5 with a protein kinase domain (PFAM Accession No. PF00069). A single domain was found, with a bit score of 350.2 and an E-value of 2.3e-101. Fig. [6B] 4B depicts an alignment of amino acid residues 356 to 613 of SEQ ID NO:5 with a serine/threonine kinase domain (SMART Accession No. S_TKc). The bit score is 372.7 and the E-value is 3.8e-108. Fig. [6C] 4C depicts an alignment of amino acid residues 356 to 613 of SEQ ID NO:5 with a tyrosine kinase domain (SMART Accession No. TyrKc). The bit score is 50.0 and the E-value is 5.3e-15. All three alignments show an underlined sequence at 473 to 485, which is a pattern match to a serine/threonine protein kinase active site signature sequence (Prosite Accession No. PS00108).